

Peak Data										Normalized Peak Area							
No.	Label	Size	Ref. size	Size diff.	MRC size	Height	Width	Area	Peak Area	Ref. Mean	Ref. SD	Ref. Weigh	Position p-tel band	Dist. Ratio	1.0 in SD	low high	
16	64 -	60.35	60.50	-0.15	64	955	12.8	12179	1.461	1.397	0.154	1.03	64 nt	1.05	0.4	.	
17	70 -	66.52	66.54	-0.02	70	607	8.8	5360	0.643	0.731	0.080	1.04	70 nt	0.88	-1.1	.	
19	76 -	72.72	72.86	-0.14	76	669	10.0	6703	0.804	0.917	0.080	1.30	76 nt	0.88	-1.4	.	
20	82 -	79.26	79.26	0.00	82	709	12.8	9098	1.092	0.943	0.169	0.63	82 nt	1.16	0.9	-.	
Ctrl: Q-fragments					Mean	735	11.1	8335	1.000	0.997	0.121	1.00	(CV: 0.13)	0.97			
22	6 a	85.58	85.67	-0.09	88	3099	5.2	16204	0.866	1.276	0.895	0.35	6p21.3 CpG isl.	0.68	-0.5	.	
23	2 a	90.92	91.04	-0.12	92	3666	5.4	19860	1.061	0.882	0.168	1.28	2q14 synt.	1.20	1.1	-.	
25	1 a	96.98	97.09	-0.11	96	3367	5.8	19628	1.049	1.023	0.182	1.37	mv36 1p36.3 CpG isl.	1.03	0.1	.	
Ctrl: D-fragments					Mean	3377	5.5	18564	0.992	1.060	0.415	1.00	(CV: 0.19)	1.06			
26	X a	100.79	100.93	-0.14	100	2321	5.3	12409	0.663	0.541	0.118	0.66	111.94 Xq23	1.23	1.0	-.	
27	Y a	105.31	105.46	-0.15	105	2947	5.5	16122	0.862	0.828	0.089	1.34	13.98 Yq11.21	1.04	0.4	.	
Ctrl: X- & Y-fragments (male ref.)					Mean	2634	5.4	14266	0.762	0.685	0.103	1.00	(CV: 0.11)	1.10			
29	5 A	124.46	124.53	-0.07	128	2711	5.6	15092	0.806	0.791	0.068	0.87	5q31.1	1.02	0.2	.	
37	3 A	171.66	171.72	-0.06	172	4076	5.4	21990	1.175	1.284	0.106	0.91	3p22	0.91	-1.0	.	
44	2 A	208.42	208.42	0.00	208	3392	5.6	19153	1.023	0.999	0.132	0.57	2p13	1.02	0.2	.	
47	12 A	225.68	225.69	-0.01	226	3239	5.7	18619	0.995	0.925	0.092	0.75	12q24	1.08	0.8	-.	
67	2 B	382.07	382.08	-0.01	382	2206	7.1	15753	0.975	1.018	0.060	1.27	2p16	0.96	-0.7	.	
74	13 B	443.78	443.75	0.03	445	2343	7.8	18324	1.134	1.018	0.077	0.99	13q34	1.11	1.5	-.	
76	2 B	460.03	459.98	0.05	463	2046	7.8	15872	0.982	0.954	0.044	1.63	2p21	1.03	0.6	.	
77	3 B	471.47	471.51	-0.04	472	1784	8.2	14672	0.908	1.009	0.075	1.01	3p21	0.90	-1.3	.	
Reference fragments					Mean	2725	6.7	17434	1.000	1.000	0.082	1.00	(CV: 0.07)	1.00			
66	7 b	372.50	372.53	-0.03	373	1621	7.0	11266	0.697	0.756	0.085	0.76	55.2 EGFR ex 1	0.92	-0.7	.	
71	7 b	417.79	417.75	0.04	418	2121	7.3	15462	0.957	1.090	0.066	1.41	55.2 EGFR ex 2	0.88	-2.0	.	
68	7 b	390.02	389.98	0.04	391	3092	7.1	22042	1.364	1.289	0.139	0.79	55.2 EGFR ex 3	1.06	0.5	-.	
58	7 b	309.25	309.29	-0.04	310	3772	6.4	24246	1.501	1.607	0.137	1.00	55.2 EGFR ex 4	0.93	-0.8	.	
33	7 a	153.90	153.92	-0.02	154	5091	5.4	27574	1.473	1.423	0.117	1.04	55.2 EGFR ex 5	1.04	0.4	.	
30	7 a	132.28	132.31	-0.03	136	4976	5.4	26850	1.435	1.486	0.110	1.15	55.2 EGFR ex 6	0.97	-0.5	.	
39	7 a	184.06	184.10	-0.04	184	3674	5.6	20531	1.097	0.914	0.083	0.94	55.2 EGFR ex 7	1.20	2.2	-.	
72	7 b	426.29	426.23	0.06	427	2128	7.3	15438	0.956	1.053	0.105	0.86	55.2 EGFR ex 8	0.91	-0.9	.	
45	7 a	214.57	214.50	0.07	214	3745	5.8	21607	1.155	1.068	0.061	1.49	55.2 EGFR ex 13	1.08	1.4	-.	
75	7 b	452.27	452.24	0.03	454	4073	7.8	31765	1.966	1.614	0.252	0.55	55.2 EGFR ex 16	1.22	1.4	-.	
49	7 a	238.07	238.06	0.01	238	5252	5.8	30384	1.624	1.531	0.129	1.01	55.2 EGFR ex 22	1.06	0.7	-.	
7p11.2 EGFR					Mean	3595	6.4	22470	1.293	1.257	0.117	1.00	(CV: 0.11)	1.01			
42	9 a	202.16	202.15	0.01	202	4591	5.9	26894	1.437	1.351	0.193	0.83	22.0 CDKN2A ex 2	1.06	0.4	-.	
53	9 b	271.43	271.46	-0.03	274	2754	6.2	17022	1.054	1.137	0.089	1.52	22.0 CDKN2A ex 3	0.93	-0.9	.	
63	9 b	355.65	355.75	-0.10	355	1512	6.8	10257	0.635	0.772	0.104	0.88	22.0 CDKN2A Int 1	0.82	-1.3	.	
52	9 a	264.01	263.98	0.03	265	1951	5.9	11544	0.715	0.802	0.095	1.00	22.0 CDKN2A Pro A	0.89	-0.9	.	
34	9 a	161.02	161.06	-0.04	160	1610	5.6	8987	0.480	0.551	0.084	0.78	22.0 CDKN2A Pro B	0.87	-0.8	.	
9p21 CDKN2A					Mean	2484	6.1	14941	0.864	0.923	0.113	1.00	(CV: 0.09)	0.92			
55	10 b	291.30	291.29	0.01	292	2634	6.4	16768	1.038	1.125	0.102	1.19	89.7 PTEN ex 1A	0.92	-0.8	.	
60	10 b	327.72	327.81	-0.09	328	2773	6.5	18098	1.120	1.316	0.118	1.21	89.7 PTEN ex 1B	0.85	-1.7	.	
61	10 b	338.58	338.70	-0.12	337	2826	6.6	18759	1.161	1.202	0.071	1.82	89.7 PTEN ex 2A	0.97	-0.6	.	
40	10 a	189.59	189.61	-0.02	190	4012	5.8	23439	1.253	1.406	0.141	1.08	89.7 PTEN ex 2B	0.89	-1.1	.	
38	10 a	177.82	177.94	-0.12	178	2938	5.5	16020	0.856	0.936	0.167	0.61	89.7 PTEN ex 3	0.91	-0.5	.	
48	10 a	230.74	230.77	-0.03	232	3166	5.9	18665	0.997	1.097	0.131	0.90	89.7 PTEN ex 4	0.91	-0.8	.	
64	10 b	363.49	363.56	-0.07	364	1752	6.7	11757	0.728	0.820	0.146	0.61	89.7 PTEN ex 5	0.89	-0.6	.	
59	10 b	319.01	319.05	-0.04	319	2527	6.5	16365	1.013	0.978	0.126	0.84	89.7 PTEN ex 6	1.04	0.3	.	
32	10 a	146.96	147.07	-0.11	148	2890	5.5	15793	0.844	0.880	0.119	0.80	89.7 PTEN ex 7	0.96	-0.3	.	
69	10 b	399.37	399.32	0.05	400	1652	7.3	12011	0.743	0.828	0.101	0.89	89.7 PTEN ex 8	0.90	-0.8	.	
73	10 b	434.96	434.92	0.04	436	2126	7.6	16242	1.005	1.079	0.112	1.04	89.7 PTEN ex 9	0.93	-0.7	.	
10q23.3 PTEN					Mean	2663	6.4	16720	0.978	1.060	0.121	1.00	(CV: 0.05)	0.93			
57	17 b	301.56	301.59	-0.03	301	4497	6.2	27966	1.731	1.492	0.243	0.72	7.6 TP53 ex 1A	1.16	1.0	-.	
35	17 a	166.36	166.50	-0.14	166	4031	5.5	21986	1.175	1.142	0.110	1.21	7.6 TP53 ex 1B	1.03	0.3	.	
41	17 a	195.96	195.96	0.00	196	3103	5.7	17705	0.946	0.865	0.099	1.03	7.6 TP53 ex 2	1.09	0.8	-.	
46	17 a	220.50	220.47	0.03	220	2729	5.8	15746	0.841	0.776	0.084	1.08	7.6 TP53 ex 4	1.08	0.8	-.	
50	17 a	246.79	246.82	-0.03	247	2346	6.0	14184	0.758	0.716	0.061	1.37	7.6 TP53 ex 5	1.06	0.7	-.	
51	17 a	253.68	253.66	0.02	256	2534	6.0	15149	0.810	0.750	0.081	1.09	7.6 TP53 ex 6	1.08	0.7	-.	
54	17 b	280.56	280.53	0.03	283	3147	6.3	19700	1.219	1.191	0.184	0.76	7.6 TP53 ex 8	1.02	0.2	.	
62	17 b	345.55	345.66	-0.11	346	2157	6.8	14634	0.906	0.869	0.136	0.75	7.6 TP53 ex 11	1.04	0.3	.	
17p13.1 TP53					Mean	3068	6.0	18384	1.048	0.975	0.125	1.00	(CV: 0.04)	1.07			
31	17 a	140.29	140.28	0.01	142	3640	5.3	19397	1.037	1.024	0.068	1.18	35.1 ERBB2 ex 1A	1.01	0.2	.	
70	17 b	407.86	407.81	0.05	409	1898	7.4	14094	0.872	0.944	0.089	0.82	35.1 ERBB2 ex 1B	0.92	-0.8	.	
17q21.1 ERBB2					Mean	2769	6.4	16746	0.954	0.984	0.079	1.00	(CV: 0.06)	0.98			

Peak Data										Normalized Peak Area					
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Mean values				-0.02		3009	6.3	18550	1.070	1.078	0.117	5		0.98	Total of all except
Standard deviations				0.06		(Coef. of variance: 0.310)			0.325	0.277				0.09	Ctrl and '?' peaks
Quality assessment						Quality limits			Quality						
Mean A-group area / mean Q-frag. area						>0.40 (1.00)			2.25						
Mean CpG-area / mean A-group area						>0.30 (0.65)			0.96						
Mean height of first probes A						> 450 (700)			3355						
Mean height of last probes B						> 190 (400)			2095						
Ratio of mean heights A/B ('slope')						<3.50 (2.50)			1.60						
CV of Control Probes						<0.75 (0.40)			0.07						
6 unidentified peak areas / 50 peak areas						< (0.02)			0.00						

Weighted mean ratios are tested for being outside ratio 1 ± 0.13
One-tailed significance is high for $p \leq 1\%$, and low for $p \leq 5\%$.
Individual peaks having normalized area > 4.0 SD from the ref.
mean and ratio < 0.65 or > 1.3 indicate 'abnormal' probe area.

Female & male ref.
Normal probes

An "*" marks: Size Diff. >0.5 , Peak Height >7000 , unexpected peak width, and "Dist. in SD" >4.0 .
Ratio group mean and coefficient of variance (CV) are weighted by the ref. weights
Labels A,B,... define normalization groups; a,b,... labeled probes do not contribute to normalization.
Mean Rox height is 457 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.07

(Ctrl probes are used for quality evaluation only)